

Amendments to the Specification:

Please amend the paragraph at page bridging page 6, line 21 to page 7, line 14 to read as follows:

-- Other modified polypeptides that are useful in the instant invention are variants or fragments of these proteins that share the biological activity of the mature (*i.e.*, unmodified) human IL-18 protein. As defined herein, such variants include modified proteins also characterized by alterations made in the known amino sequence of the proteins. Such variants are characterized by having an amino acid sequence differing from that of the mature protein by eight or fewer amino acid residues, and, preferably, by about five or fewer residues. In one embodiment of the invention, any differences in the amino acid sequences of the proteins involve only conservative amino acid substitutions. Conservative amino acid substitutions occur when an amino acid has substantially the same charge as the amino acid for which it is substituted and the substitution has no significant effect on the local conformation of the protein or its biological activity. Alternatively, changes such as the introduction of a certain amino acid in the sequence which may alter the stability of the protein, or permit it to be expressed in a desired host cell, may be preferred. Moreover, variation in primary amino acid sequence with no substantial change in protein structure and function are known in this art. Such variants are readily detected and predicted by algorithms used by those skilled in this art. For example, the well known BLAST algorithm (Altschul, S. F., *et al.* (1990) *J. Mol. Biol.* 215:403-410) utilizes an amino acid substitution matrix to predict and evaluate tolerable amino acid substitution at residues of the query sequence. Accordingly, the skilled artisan appreciates the scope and meaning of the term "variant" when used to describe equivalent embodiments of a given polypeptide sequence. The term, "substitution mutant," as used herein, means a protein in which an amino acid residue is replaced with another amino acid residue. A human IL-18 "substitution mutant," as used herein, means a mutant that comprises from one to five amino acid substitutions in the sequence of SEQ ID NO:1, said substitutions being at an amino acid residue chosen from the group of: the cysteine at residue 38, the cysteine at residue 68, the cysteine at residue 76, the asparagine at residue 78, the glutamic acid at residue 121, the cysteine at residue 127, the leucine at residue 144, and the aspartic acid at residue 157. --